

# SEQUENCE LISTING

<110> Sewalt, Vincent J. H.  
Jung, Rudolf  
Hu, Wang-Nan  
Meeley, Robert B.

<120> Improved Grain Quality Through Altered  
Expression of Seed Proteins

<130> 1276

<150> US 60/246,455

<151> 2000-11-07

<160> 10

<170> FastSEQ for Windows Version 3.0

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<212> DNA

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<220>

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<222> (120)...(1004)

<223> 50 kD gamma-zein prolamin/PTA 2272

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atg aag ctg gtg ctt gtg gtt ctt gct ttc att gct tta gta tca agt	167
Met Lys Leu Val Leu Val Val Leu Ala Phe Ile Ala Leu Val Ser Ser	
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ggt tct tgt aca cag aca ggc ggc tgc agc tgt ggt caa caa caa agc	215
Val Ser Cys Thr Gln Thr Gly Gly Cys Ser Cys Gly Gln Gln Ser	
20 25 30	
cat gag cag caa cat cat cca caa caa cat cat cca caa aaa caa caa	263
His Glu Gln Gln His His Pro Gln Gln His His Pro Gln Lys Gln Gln	
35 40 45	
cat caa cca cca cca caa cat cac cag cag cag caa cac caa caa caa	311
His Gln Pro Pro Pro Gln His His Gln Gln Gln Gln His Gln Gln Gln	
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caa gtt cac atg caa cca caa aaa cat cag caa caa caa gaa gtt cat	359
Gln Val His Met Gln Pro Gln Lys His Gln Gln Gln Gln Glu Val His	
65 70 75 80	
ggt caa caa caa caa caa caa ccg cag cac caa caa caa caa caa caa	407
Val Gln Gln Gln Gln Gln Gln Pro Gln His Gln Gln Gln Gln Gln	

85	90	95	
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Gln Gln His Gln Gln Gln His	Gln Cys Glu Gly Gln Gln Gln His His		
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caa caa tca caa ggc cat gtg	caa caa cac gaa cag agc cat gag caa		503
Gln Gln Ser Gln Gly His Val	Gln Gln His Glu Gln Ser His Glu Gln		
115	120	125	
cac caa gga cag agc cat gag	caa caa cat caa caa caa ttc cag ggt		551
His Gln Gly Gln Ser His	Gln Gln Gln His Gln Gln Phe Gln Gly		
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cat gac aag cag caa caa cca	caa cag cct cag caa tat cag cag ggc		599
His Asp Lys Gln Gln Gln Pro	Gln Gln Pro Gln Gln Tyr Gln Gln Gly		
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cag gaa aaa tca caa cag caa	caa tgt cat tgc cag gag cag caa cag		647
Gln Glu Lys Ser Gln Gln Gln	Gln Cys His Cys Gln Glu Gln Gln Gln		
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act aca agg tgc agc tat aac	tac tat agc agt agc tca aat cta aaa		695
Thr Thr Arg Cys Ser Tyr Asn	Tyr Tyr Ser Ser Ser Ser Asn Leu Lys		
180	185	190	
aat tgt cat gaa ttc cta agg	cag cag tgc agc cct ttg gta atg cct		743
Asn Cys His Glu Phe Leu Arg	Gln Gln Cys Ser Pro Leu Val Met Pro		
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ttt ctc caa tca cgt ttg ata	caa cca agt agc tgc cag gta ttg cag		791
Phe Leu Gln Ser Arg Leu Ile	Gln Pro Ser Ser Cys Gln Val Leu Gln		
210	215	220	
caa caa tgt tgt cat gat ctt	agg cag att gag cca caa tac att cac		839
Gln Gln Cys Cys His Asp Leu	Arg Gln Ile Glu Pro Gln Tyr Ile His		
225	230	235	240
caa gca atc tac aac atg gtt	caa tcc ata atc cag gag gag caa caa		887
Gln Ala Ile Tyr Asn Met Val	Gln Ser Ile Ile Gln Glu Glu Gln Gln		
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Gln Gln Pro Cys Glu Leu Cys	Gly Ser Gln Gln Ala Thr Pro Lys Cys		
260	265	270	
ggg ggc aat ctt gac agc agc	aca ata cct acc atc aat gtg cgg ctt		983
Gly Gly Asn Leu Asp Ser Ser	Thr Ile Pro Thr Ile Asn Val Arg Leu		
275	280	285	
gta cca ctc ata cta cca aaa	taatccatgc agcagcaatg acattagtgg		1034
Val Pro Leu Ile Leu Pro Lys			
290	295		
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ataaagtacc atacattatg atgttaaaaa	aaaaa		1129

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 <212> PRT  
 <213> Zea mays

<400> 2

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Val	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Gln	His	Gln	Gln	Gln	Gln	Gln	Gln
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Gln	Gln	His	Gln	Gln	Gln	His	Gln	Cys	Glu	Gly	Gln	Gln	Gln	His	His
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His	Asp	Lys	Gln	Gln	Gln	Pro	Gln	Gln	Pro	Gln	Gln	Tyr	Gln	Gln	Gly
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Gln	Glu	Lys	Ser	Gln	Gln	Gln	Gln	Cys	His	Cys	Gln	Glu	Gln	Gln	Gln
				165				170						175	
Thr	Thr	Arg	Cys	Ser	Tyr	Asn	Tyr	Tyr	Ser	Ser	Ser	Ser	Asn	Leu	Lys
			180					185					190		
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225					230					235					240
Gln	Ala	Ile	Tyr	Asn	Met	Val	Gln	Ser	Ile	Ile	Gln	Glu	Glu	Gln	Gln
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Gln	Gln	Pro	Cys	Glu	Leu	Cys	Gly	Ser	Gln	Gln	Ala	Thr	Pro	Lys	Cys
			260					265					270		
Gly	Gly	Asn	Leu	Asp	Ser	Ser	Thr	Ile	Pro	Thr	Ile	Asn	Val	Arg	Leu
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	290					295									

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<220>  
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					Met Ala										
					1										
aag atc gcc	gcg gcg gcg	gcg gcg gcg	gcg gcg gcg	ctg tgc ttc	gcg gcc ctg	gtg									164
Lys Ile Ala	Ala Ala Ala	Ala Ala Ala	Ala Ala Ala	Leu Cys Phe	Ala Ala Leu	Val									
	5		10		15										
gcc gtg gcc	gtc tgc caa	ggc gag gtc	gag cgg cag	agg ctc agg	gac										212
Ala Val Ala	Val Cys Gln	Gly Glu Val	Glu Arg Gln	Arg Leu Arg	Asp										
	20		25		30										
ctg cag tgc	tgg cag gag	gtc cag gag	agc ccg ctc	gac gcg tgc	cgc										260
Leu Gln Cys	Trp Gln Glu	Val Gln Glu	Ser Pro Leu	Asp Ala Cys	Arg										
	35		40		45										
cag gtc ctc	gac cgg cag	cta acc ggc	ggc ggc ggc	ggc ggc ggc	ggc ggc ggc	gtt									308
Gln Val Leu	Asp Arg Gln	Leu Thr Gly	Gly Gly Gly	Gly Gly Gly	Gly Gly Gly	Val									
		55		60		65									
ggc ccg ttc	cgg tgg ggc	acc ggg ctc	cgg atg cgg	tgc tgc cag	cag										356
Gly Pro Phe	Arg Trp Gly	Thr Gly Leu	Arg Met Arg	Cys Cys Gln	Gln										
	70		75		80										
ctc cag gac	gtg agc cgc	gag tgc cgc	tgc gcc gcc	atc cgg agc	atg										404
Leu Gln Asp	Val Ser Arg	Glu Cys Arg	Cys Ala Ala	Ile Arg Ser	Met										
	85		90		95										
gtc agg ggc	tac gag gag	gcc atg ccg	ccg ctg gag	aaa ggc tgg	tgg										452
Val Arg Gly	Tyr Glu Glu	Ala Met Pro	Pro Pro Leu	Glu Lys Gly	Trp Trp										
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cca tgg ggg	cgg cag cag	cag ccg ccg	ccg cag gga	gga gga gga	gga gga gga										500
Pro Trp Gly	Arg Gln Gln	Gln Pro Pro	Pro Gln Gly	Gly Gly Gly	Gly Gly Gly										
	115		120		125										
cag ggg ggc	tac tac tac	ccc tgc agc	cgg cca gga	gag gga tac	ggc										548
Gln Gly Gly	Tyr Tyr Tyr	Pro Cys Ser	Arg Pro Gly	Glu Gly Tyr	Gly										
		135		140		145									
tac ggt cag	ggt ggc cag	cgg cag atg	tat cca ccg	tgt cgt ccc	ggc										596
Tyr Gly Gln	Gly Gly Gln	Arg Gln Met	Tyr Pro Pro	Cys Arg Pro	Gly										
	150		155		160										
acc acc ggc	ggc ggg cca	agg atc ggc	cgc gtg agg	ctt acg aag	gcc										644
Thr Thr Gly	Gly Gly Gly	Pro Arg Ile	Gly Arg Val	Arg Leu Thr	Lys Ala										
	165		170		175										
cgg gag tac	gcc gcg ggg	ttg ccg atg	atg tgc cgg	ctg tgc gag	ccc										692
Arg Glu Tyr	Ala Ala Gly	Leu Pro Met	Met Cys Arg	Leu Ser Glu	Pro										
	180		185		190										
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Gln Glu Cys	Ser Ile Phe	Ser Gly Gly	Asp Gln Tyr												

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 35 40 45  
 Cys Arg Gln Val Leu Asp Arg Gln Leu Thr Gly Gly Gly Gly Gly Gly  
 50 55 60  
 Gly Val Gly Pro Phe Arg Trp Gly Thr Gly Leu Arg Met Arg Cys Cys  
 65 70 75 80  
 Gln Gln Leu Gln Asp Val Ser Arg Glu Cys Arg Cys Ala Ala Ile Arg  
 85 90 95  
 Ser Met Val Arg Gly Tyr Glu Glu Ala Met Pro Pro Leu Glu Lys Gly  
 100 105 110  
 Trp Trp Pro Trp Gly Arg Gln Gln Gln Pro Pro Pro Gln Gly Gly Gly  
 115 120 125  
 Gly Gly Gln Gly Gly Tyr Tyr Tyr Pro Cys Ser Arg Pro Gly Glu Gly  
 130 135 140  
 Tyr Gly Tyr Gly Gln Gly Gly Gln Arg Gln Met Tyr Pro Pro Cys Arg  
 145 150 155 160  
 Pro Gly Thr Thr Gly Gly Gly Pro Arg Ile Gly Arg Val Arg Leu Thr  
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 Lys Ala Arg Glu Tyr Ala Ala Gly Leu Pro Met Met Cys Arg Leu Ser  
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Ser	Gly	Gln	Val	Arg	Pro	Leu	Pro	Ser	Ser	Leu	Pro	Leu	Ser	Leu	Leu	
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Leu	Leu	Leu	Leu	Leu	Cys	Cys	Ser	Gly	Thr	Ser	Trp	Gly	Trp	Ser	Thr	
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tcc	cgg	gga	gga	gcc	gcc	agg	gag	tgc	ggc	ttc	gat	ggc	aag	ctg	gag	198
Ser	Arg	Gly	Gly	Ala	Ala	Arg	Glu	Cys	Gly	Phe	Asp	Gly	Lys	Leu	Glu	
40					45				50					55		
gcc	ctg	gag	ccg	cgc	cac	aag	gtg	cag	tct	gag	gcc	ggc	tcc	gtc	cag	246
Ala	Leu	Glu	Pro	Arg	His	Lys	Val	Gln	Ser	Glu	Ala	Gly	Ser	Val	Gln	
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tac	ttc	agc	cgg	ttc	aac	gaa	gcc	gac	cgg	gag	ctc	acc	tgc	gcc	ggc	294
Tyr	Phe	Ser	Arg	Phe	Asn	Glu	Ala	Asp	Arg	Glu	Leu	Thr	Cys	Ala	Gly	
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atc	ttc	gcc	gtc	cgc	gtc	gtc	gtc	gac	gcc	atg	ggc	ctc	ctg	ctc	cct	342
Ile	Phe	Ala	Val	Arg	Val	Val	Val	Asp	Ala	Met	Gly	Leu	Leu	Leu	Pro	
		90					95					100				
cga	tac	tcc	aac	gtc	cat	tcg	ctt	gtc	tac	atc	gtc	caa	ggg	aga	ggg	390
Arg	Tyr	Ser	Asn	Val	His	Ser	Leu	Val	Tyr	Ile	Val	Gln	Gly	Arg	Gly	
	105					110					115					
atc	att	ggg	ttc	tcg	ttt	ccg	gga	tgc	caa	gag	gag	acc	cag	cag	cag	438
Ile	Ile	Gly	Phe	Ser	Phe	Pro	Gly	Cys	Gln	Glu	Glu	Thr	Gln	Gln	Gln	
120					125				130					135		
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Gln	Tyr	Gly	Tyr	Gly	Tyr	Gly	Tyr	Gly	His	His	His	His	Gln	His	Asp	
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cac	cac	aag	atc	cac	cga	ttc	gag	cag	ggc	gac	gtg	gtg	gcc	atg	ccg	534
His	His	Lys	Ile	His	Arg	Phe	Glu	Gln	Gly	Asp	Val	Val	Ala	Met	Pro	
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gcc	ggc	gcc	cag	cac	tgg	ctg	tac	aac	gac	ggc	gac	gcg	ccg	ctt	gtg	582
Ala	Gly	Ala	Gln	His	Trp	Leu	Tyr	Asn	Asp	Gly	Asp	Ala	Pro	Leu	Val	
		170					175					180				
gcg	gtc	tac	gtc	ttc	gac	gag	aac	aac	aac	atc	aac	cag	ctc	gag	cct	630
Ala	Val	Tyr	Val	Phe	Asp	Glu	Asn	Asn	Asn	Ile	Asn	Gln	Leu	Glu	Pro	
	185					190					195					
tcc	atg	agg	aaa	ttt	ttg	ctg	gct	ggg	ggc	ttc	agc	aag	ggg	cag	ccc	678
Ser	Met	Arg	Lys	Phe	Leu	Leu	Ala	Gly	Gly	Phe	Ser	Lys	Gly	Gln	Pro	
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His	Phe	Ala	Glu	Asn	Ile	Phe	Lys	Gly	Ile	Asp	Ala	Arg	Phe	Leu	Ser	
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gaa	gcc	ctg	ggc	gtc	agc	atg	cac	gtc	gcc	gag	aag	ctg	cag	agc	cgg	774

Glu	Ala	Leu	Gly	Val	Ser	Met	His	Val	Ala	Glu	Lys	Leu	Gln	Ser	Arg	
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His	Gln	Leu	Asn	Pro	Ser	Pro	Ser	Ser	Ser	Ser	Phe	Ser	Phe	Pro	Ser	
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Ser	Gln	Val	Gln	Tyr	Gln	Thr	Cys	Gln	Arg	Asp	Val	Asp	Arg	His	Asn	
280					285					290					295	
gtc	tgc	gcc	atg	gag	gtg	agg	cac	agc	gtc	gaa	cgg	ctg	gac	cag	gcc	966
Val	Cys	Ala	Met	Glu	Val	Arg	His	Ser	Val	Glu	Arg	Leu	Asp	Gln	Ala	
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gac	gtc	tac	agc	cct	ggg	gct	ggg	agg	atc	aca	cgc	ctc	acc	agc	cac	1014
Asp	Val	Tyr	Ser	Pro	Gly	Ala	Gly	Arg	Ile	Thr	Arg	Leu	Thr	Ser	His	
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aag	ttc	ccc	gtc	ctc	aac	ctc	gta	cag	atg	agc	gcg	gtg	cgg	gta	gac	1062
Lys	Phe	Pro	Val	Leu	Asn	Leu	Val	Gln	Met	Ser	Ala	Val	Arg	Val	Asp	
		330					335					340				
ctg	tac	cag	gac	gcc	atc	atg	tcg	ccg	ttc	tgg	aac	ttc	aac	gcc	cac	1110
Leu	Tyr	Gln	Asp	Ala	Ile	Met	Ser	Pro	Phe	Trp	Asn	Phe	Asn	Ala	His	
	345					350					355					
agc	gcc	atg	tac	ggc	atc	agg	ggc	agt	gca	agg	gtc	cag	gtc	gcc	agc	1158
Ser	Ala	Met	Tyr	Gly	Ile	Arg	Gly	Ser	Ala	Arg	Val	Gln	Val	Ala	Ser	
360					365					370					375	
gac	aac	ggg	acc	acg	gtg	ttc	gac	gac	gtg	ctc	cgt	gcg	ggg	cag	ctg	1206
Asp	Asn	Gly	Thr	Thr	Val	Phe	Asp	Asp	Val	Leu	Arg	Ala	Gly	Gln	Leu	
				380					385					390		
ctc	atc	gta	ccc	cag	ggc	tac	ctc	gtc	gcc	acc	aag	gcg	cag	gga	gaa	1254
Leu	Ile	Val	Pro	Gln	Gly	Tyr	Leu	Val	Ala	Thr	Lys	Ala	Gln	Gly	Glu	
			395					400					405			
ggc	ttc	cag	tac	atc	gcc	ttc	gag	acg	aac	cct	gac	acc	atg	gtc	agc	1302
Gly	Phe	Gln	Tyr	Ile	Ala	Phe	Glu	Thr	Asn	Pro	Asp	Thr	Met	Val	Ser	
		410					415					420				
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His	Val	Ala	Gly	Lys	Asn	Ser	Val	Leu	Ser	Asp	Leu	Pro	Ala	Ala	Val	
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atc	gcc	agc	tcg	tat	gcc	atc	tcc	atg	gag	gaa	gct	gca	gag	ctc	aag	1398
Ile	Ala	Ser	Ser	Tyr	Ala	Ile	Ser	Met	Glu	Glu	Ala	Ala	Glu	Leu	Lys	
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aac	ggt	agg	aag	cat	gag	ctg	gct	gtg	ctt	act	cct	gct	ggc	agt	ggc	1446

Asn Gly Arg Lys His Glu Leu Ala Val Leu Thr Pro Ala Gly Ser Gly  
460 465 470

agc tac caa caa ggt caa gct ggc agc gcc caa cag tag gcacaacctc 1495  
Ser Tyr Gln Gln Gly Gln Ala Gly Ser Ala Gln Gln \*  
475 480

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Thr	Ser	Trp	Gly	Trp	Ser	Thr	Ser	Arg	Gly	Gly	Ala	Ala	Arg	Glu	Cys	35	40	45	
Gly	Phe	Asp	Gly	Lys	Leu	Glu	Ala	Leu	Glu	Pro	Arg	His	Lys	Val	Gln	50	55	60	
Ser	Glu	Ala	Gly	Ser	Val	Gln	Tyr	Phe	Ser	Arg	Phe	Asn	Glu	Ala	Asp	65	70	75	80
Arg	Glu	Leu	Thr	Cys	Ala	Gly	Ile	Phe	Ala	Val	Arg	Val	Val	Val	Asp	85	90	95	
Ala	Met	Gly	Leu	Leu	Pro	Arg	Tyr	Ser	Asn	Val	His	Ser	Leu	Val		100	105	110	
Tyr	Ile	Val	Gln	Gly	Arg	Gly	Ile	Ile	Gly	Phe	Ser	Phe	Pro	Gly	Cys	115	120	125	
Gln	Glu	Glu	Thr	Gln	Gln	Gln	Gln	Tyr	Gly	Tyr	Gly	Tyr	Gly	Tyr	Gly	130	135	140	
His	His	His	His	Gln	His	Asp	His	His	Lys	Ile	His	Arg	Phe	Glu	Gln	145	150	155	160
Gly	Asp	Val	Val	Ala	Met	Pro	Ala	Gly	Ala	Gln	His	Trp	Leu	Tyr	Asn	165	170	175	
Asp	Gly	Asp	Ala	Pro	Leu	Val	Ala	Val	Tyr	Val	Phe	Asp	Glu	Asn	Asn	180	185	190	
Asn	Ile	Asn	Gln	Leu	Glu	Pro	Ser	Met	Arg	Lys	Phe	Leu	Leu	Ala	Gly	195	200	205	
Gly	Phe	Ser	Lys	Gly	Gln	Pro	His	Phe	Ala	Glu	Asn	Ile	Phe	Lys	Gly	210	215	220	
Ile	Asp	Ala	Arg	Phe	Leu	Ser	Glu	Ala	Leu	Gly	Val	Ser	Met	His	Val	225	230	235	240
Ala	Glu	Lys	Leu	Gln	Ser	Arg	Arg	Asp	Gln	Arg	Gly	Glu	Ile	Val	Arg	245	250	255	
Val	Glu	Pro	Glu	His	Gly	Phe	His	Gln	Leu	Asn	Pro	Ser	Pro	Ser	Ser	260	265	270	
Ser	Ser	Phe	Ser	Phe	Pro	Ser	Ser	Gln	Val	Gln	Tyr	Gln	Thr	Cys	Gln	275	280	285	
Arg	Asp	Val	Asp	Arg	His	Asn	Val	Cys	Ala	Met	Glu	Val	Arg	His	Ser	290	295	300	



Val Glu Arg Leu Asp Gln Ala Asp Val Tyr Ser Pro Gly Ala Gly Arg  
 305 310 315 320  
 Ile Thr Arg Leu Thr Ser His Lys Phe Pro Val Leu Asn Leu Val Gln  
 325 330 335  
 Met Ser Ala Val Arg Val Asp Leu Tyr Gln Asp Ala Ile Met Ser Pro  
 340 345 350  
 Phe Trp Asn Phe Asn Ala His Ser Ala Met Tyr Gly Ile Arg Gly Ser  
 355 360 365  
 Ala Arg Val Gln Val Ala Ser Asp Asn Gly Thr Thr Val Phe Asp Asp  
 370 375 380  
 Val Leu Arg Ala Gly Gln Leu Leu Ile Val Pro Gln Gly Tyr Leu Val  
 385 390 395 400  
 Ala Thr Lys Ala Gln Gly Glu Gly Phe Gln Tyr Ile Ala Phe Glu Thr  
 405 410 415  
 Asn Pro Asp Thr Met Val Ser His Val Ala Gly Lys Asn Ser Val Leu  
 420 425 430  
 Ser Asp Leu Pro Ala Ala Val Ile Ala Ser Ser Tyr Ala Ile Ser Met  
 435 440 445  
 Glu Glu Ala Ala Glu Leu Lys Asn Gly Arg Lys His Glu Leu Ala Val  
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 Ala Gln Gln

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 <212> DNA  
 <213> Zea mays

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 <221> allele  
 <222> (0)...(0)  
 <223> 50kD gamma-zein, B73 partial

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 acaacagcac caacaacaac atcaatgtga aggccaacaa caacatcacc aacaatcaca 180  
 aggccatgtg caacaacacg aacagagcca tgagcaacac caaggacaga gccatgagca 240  
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 <212> DNA  
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<220>  
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 <222> (0)...(0)  
 <223> 50kD gamma-zein, Mo17 partial

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 acaagaagtt catgttcaac aacaacaaca acaaccgcag caccaacaac aacaacaaca 120

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ccatgtgcaa	caacacgaac	agagccatga	gcaacaccaa	ggacagagcc	atgagcaaca	240
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tcagcagggc	caggaaaaat	c				321

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 <211> 561  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> allele  
 <222> (0)...(0)  
 <223> 18 kD alpha-globulin, B73, partial

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ctcctggggc	tccgacagcc	ggcacatcat	cggcaacccc	gcggcgctact	cccgggcctt	180
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atacatctgc	cgctggccac	cctgaccgta	gccgtatccc	tctcctggcc	ggctgcaggg	300
gtagtagtag	ccccctgtc	ctcctcctcc	tccttgcggc	ggcggtgctg	gctgccgccc	360
ccatggccac	cagcctttct	ccagcggcgg	catggcctcc	tcgtagcccc	tgaccatgct	420
ccggatggcg	gcgacagcgg	actcgcggct	cacgtcctgg	agctgctggc	agcaccgcat	480
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ctgccggtcg	aggaaagggc	g				561

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 <211> 537  
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<220>  
 <221> allele  
 <222> (0)...(0)  
 <223> 18 kD alpha-globulin, Mo17 partial

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ctgtcctcct	cctcctcctc	gcggcgccgg	ctgctgctgc	cgcccccatg	gccaccagcc	360
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